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Db 121 GGRGAFGRGAEYVISPJNAPAAQNRSGAHLQRRVGGPDSPTSRGCVASGM 180
Oy 181 NPAILRALDPPRRRGGESRRRRSGAKRPFVSPRVELLVVADESMVFRGADLEH 240
Db 181 NPAILRALDPPRRRGGESRRRRSGAKRPFVSPRVELLVVADESMVFRGADLEH 240
Oy 241 YLLTLTAARLYRHPSTLNPINIVVAVKLLLRDRDSGPKVGNALFTRNCAWOKLN 300
Db 241 YLLTLTAARLYRHPSTLNPINIVVAVKLLLRDRDSGPKVGNALFTRNCAWOKLN 300
Oy 301 KVSQKHPEVMDALFTFRDGLGATTCDTLGMADVTCMDPRSCSVIEDDGLPSAFTTA 360
Db 301 KVSQKHPEVMDALFTFRDGLGATTCDTLGMADVTCMDPRSCSVIEDDGLPSAFTTA 360
Oy 361 HELGHVFNPHDNNVCEVFGKLRANHMSPTLIOIDRANWMSAALTIDFDSHG 420
Db 361 HELGHVFNPHDNNVCEVFGKLRANHMSPTLIOIDRANWMSAALTIDFDSHG 420
Oy 421 DCLLDOPSKPISLPEDLPASVYTLSSQCELAFGVSGKPCPYMQCTKLMCTGAKGOMVC 480
Db 421 DCLLDOPSKPISLPEDLPASVYTLSSQCELAFGVSGKPCPYMQCTKLMCTGAKGOMVC 480
Oy 481 QTRHFPMDGTSQSGGKCLKACVGRHNLKRVDSWAKMDPYGCSRTGCGGVOLAR 540
Db 481 QTRHFPMDGTSQSGGKCLKACVGRHNLKRVDSWAKMDPYGCSRTGCGGVOLAR 540
Oy 541 RQCTNPPTANGKGYEGVAVKYSNLEPSPSSAGSKFREDQCAFNGYNHSTRILTA 600
Db 541 RQCTNPPTANGKGYEGVAVKYSNLEPSPSSAGSKFREDQCAFNGYNHSTRILTA 600
Oy 601 VAWVKYISGVSPRDKCKLICRANGTGYVLAQVVDGTLSPDSTSVQVQKCIKACD 660
Db 601 VAWVKYISGVSPRDKCKLICRANGTGYVLAQVVDGTLSPDSTSVQVQKCIKACD 660
Oy 661 GNLGSKRRFDCGVCYGNGSKKVTGLFTKPMHGYNFVAIPGASSIDIRORCKLI 720
Db 661 GNLGSKRRFDCGVCYGNGSKKVTGLFTKPMHGYNFVAIPGASSIDIRORCKLI 720
Oy 721 GDNNTLALNSOGKYLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILLEYLT 780
Db 721 GDNNTLALNSOGKYLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILLEYLT 780
Oy 781 VEVSVGKMPRRVRYSTYLPKEPEDKSSHPKPRGVSVAHNSVLSLNOVEQPDDBRP 840
Db 781 VEVSVGKMPRRVRYSTYLPKEPEDKSSHPKPRGVSVAHNSVLSLNOVEQPDDBRP 840
Oy 841 ARWVAGSWGSPASGSGSLQKRAVDCRGSAGORTVPACDAHHPVETQAGEPPTWELS 900
Db 841 ARWVAGSWGSPASGSGSLQKRAVDCRGSAGORTVPACDAHHPVETQAGEPPTWELS 900
Oy 901 AWSPCSCKGGRFRRSLKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950
Db 901 AWSPCSCKGGRFRRSLKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950

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## RESULT 2

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Oy 91256 PRELIMINARY; PRT; 340 AA.
AC 091256;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Similar to a disintegrin and metalloproteinase with thrombospondin
DE motifs 1 (Adams-1) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC009667; AA09667.1;
DR InterPro: IPR000884; tsp1.
DR Pfam: PF00090; tsp_1; 2.
KW Integrin.
FT NON_TER 1 1
SQ SEQUENCE 340 AA; 37021 MW; 06562C747634AB8D CRC64;

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Query Match 32.6%; Score 1685; DB 11; Length 340;
Best Local Similarity 91.7%; Pred. NO. 9.5e-132;
Matches 308; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

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Oy 615 KCKLICRANGTGYFYVLAQVVDGTLSPDSTSVQVQKCIKACDGNLGSKRFPDCGV 674
Db 5 KCKLICRANGTGYFYVLAQVVDGTLCPDSTSVQVQKCIKACDGNLGSKRFPDCGV 64
Oy 675 CGDNKSKKVTGLFTKPMHGYNFVAIPAGASSIDIRORCKLIQDNTLALNSQK 734
Db 65 CGDNKSKKVTGLFTKPMHGYNFVAIPAGASSIDIRORCKLIQDNTLALNSQK 124
Oy 735 YLLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILLEYLTVEVSVMKMPRRV 794
Db 125 YLLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILLEYLTVEVSVMKMPRRV 184
Oy 795 RYSEYLPKEPEDKSSHPKPRGVSVAHNSVLSLNOVEQPDDBRPARWVAGSWGSPAS 854
Db 185 RYSEYLPKEPEDKSTRPKDRGSLVLRNSVLSLNOVEQPDDBRPARWVAGSWGSPAS 244
Oy 855 CGSLQKRAVDCRGSAGORTVPACDAHHPVETQAGEPPTWELSAWSPCSKGRGQ 914
Db 245 CGSLQKRAVDCRGSAGORTVPACDAHHPVETQAGEPPTWELSAWSPCSKGRGQ 304
Oy 915 RRSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950
Db 305 RRSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 340

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## RESULT 3

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ID 019791 PRELIMINARY; PRT; 2165 AA.
AC 019791; 027524;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F25H8.3 protein.
DE F25H8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gajdasty S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Dublin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierri-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Wellstock L., Wilkinson-Spoat J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL: Z69361; CAA93288.1;
DR EMBL: Z69360; CAA93288.1; JOINED.
DR EMBL: Z69360; CAA93287.1;
DR EMBL: Z69361; CAA93287.1; JOINED.

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Dd	148	QOSLASHRNSVALSTCGGLSGMINTTEADYFLRLRPLSHLSMKLGRMAQSSPSHYLYKR	207
QY	161	G-----VPGGSDPISR-----CGYASGNPA-----ILRA	187
Dd	208	STEPHAPGASEVLYTSRWELAHOPLHSSDLRLGLPOKOHPCGRKKRYMPDPKEDFEJIL	267
QY	188	IDPYPRRAGFGEFSRRRRSGKARFFSVIPRYVETLIVVADESMYKFPNG-ADLEHYLTLL	246
Dd	268	PBEYK-----SCLRHKRSLLRSHRNEL-----NVELIVYVDKKMMQNHNEHTYVLTIL	315
QY	247	ATAARLHRPSTLINDINIVVYKVLILDRDSDGPKVTGNAALTLRNFCAMOKUL-NKYSDK	305
Dd	320	NMYVALFFDGTIGGININIAIVGLLILDEDEOGLIASHHADTLTSCFOMOSGLMGKQTR	379
QY	306	HEPYDPTLILFRODIG--ATTQDTGMAVGMVCMOPKRCSCSYIEDGQJPSATTHL	365
Dd	380	H-----DHAILLTGLDLSWKMBPCDCLTFALISGMSCKYRSCCTJINEDGJLATTIHES	435
QY	364	GHEVNMPPHDNV-KYCEEYFGKLRANHMSPPTLIDIRANPWSACSAALITDFDLSGHDC	422
Dd	436	GHNFEMINIDEGENMCKSEG-----NIMSPILAGRNGVFSMSPCSRQYHJHFTSTAQAI	490
QY	423	LIDPSKRI-----SLPEDIJGASYLISOCELAFCVGSRCPCY---MOYCTLMC--TGKA	474
Dd	491	LADOP-KYVKEYKYPKEJLPGELIDANQCKKQPEKALCLMDEKDKIDICALMCHIRGRK	549
QY	475	KGWYVCOTRHEPMDGTSGBGSKLCLKGCACYERHNLNKHRVDSGMAKMDPYGCSRTCGG	534
Dd	550	-----CETKFMRAEGTIGCHDMCMRGQCYKCYDEGCKPTHGWSMSSMSPSCRCGG	604
QY	535	GYOLARROCTPTPANGKGYCEGVRVYKRSQNLNLPCCSSASGKFEFDEOC-----EAFNG	569
Dd	605	GVSHRSRLCTMPKSHSGKFEFGSTRTLLCLNSQKCPRDS--VDFRAQCAEHNSRRFRG	662
QY	590	YHSTNRLTLLVAVWPYKSGVSPBDCKLCLCRANGTGIFYFLAYLAVYDGLTCSPTSTVC	649
Dd	663	RHYK-----WKP-YTYVEDQDLCLYCIAGDPFFEFSLSKVADGTPCSDSNNVC	712
QY	650	VQGCIRKAGCGGNJGSKRRPKCYCGCGDNKSKCKYVGLTFKPPHH--GYNFVAIIPAGAS	707
Dd	713	IDGIERGVCGNVLGSDAVEYCVCGMGNNSACTIHGGLYTKHNHTYQYHMYTIPSGAR	772
QY	708	SIDIKORGYKGLIGDNTLALKNQSGKYLNGHFTVYSAVERDLVVKSLRLYSQGTAYE	767
Dd	773	SIRIYEMV-----STISIVRNLKRYLYNGHTVMPGR-KYFSTITTDYIRSYMEPE	826
QY	768	SLQASRPLLEPLTVEVLISVGKMTDPRVRYSEYLFKEPREDKSSHKDPGRPS-----	819
Dd	827	NLIATGPNETLIVELLFOGR--NPGVAMEWSMPR-----LGTGEKOPAPQSYTAWIVRS	879
QY	820	-----VLHNVLSLNSQVE-----QPDORP-----PARWAAGSMGPC	851
Dd	880	ECSVSCGGGQMTYVEBGCYRDLKFOYNNMFCNPKTRPTGTGLPCKVSAACPWSVSGMNSAC	939
QY	852	SASCGSGLOKRAVDC--RGSAGORTVA--CDAANRPVETQAC-GEPC-PTWELSAVSPC	905
Dd	940	SRTCGGGAOSRPGVQCTRVHNDSEPPVDSLCPQC-APSSQACQNSGCSPPRAMSAGPWAC	998
QY	906	SKSGCGRGORSLSCVGHG-----GRLARPOCNLHRRQJELDCVULARPC	950
Dd	999	SHTCGGKRRKRAVACKSTNPBARAQLLBDVAVTSEKPRMHEACLLQRC	1047

RESULT 6		
Q8SXBO		
ID	Q8SXBO	PRELIMINARY:
AC	Q8SXBO	
DT	01-JUN-2002	(TREMBlrel. 21, Created)
DT	01-JUN-2002	(TREMBlrel. 21, Last sequence update)
DT	01-JUN-2002	(TREMBlrel. 21, Last annotation update)
DE	GHI6393p.	
DN	CG6107.	



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Db 348 CVHKDEPDVGVIAVLGGVCSAKRRCVLAENGLMFLAFTIAHGLNLMNHDD-----DD 402
Oy 380 VEGKLRANMNSPTLIQIDRANP-----WSACSAIITFDLFGHGDCLL-----DPSKPS 432
Db 403 HSSCGRHSHMGEMV--GRNPDLSSSSCSRDLENFLSKYSTCLLVDPKQHTVR 460
Oy 433 LPEDLPASSTYLSQOCFAFGVSKPCPYM--CTKLMCTGKAGOMVCOYRHPPMADG 490
Db 461 LPHKRLGHMYSANECQILFGKNATFCRNMELMAGLMCL--VGDPTSCRTKLDPPLDG 518
Oy 491 TSCGSGKCLTGACVYERNNLKNHRDQSGMAKMDPYGCSRTCCGGVQALARKOCTPTPAN 550
Db 519 TEGGADKRCRAGECVSKPIPEH--VDGWSFPGAMSMCSRTCGTARPRORCDNPPGP 577
Oy 551 GKGCEGVRYVYRSCNLEPCSSASGKSFRECEAFNGYNHSTRLTLAAVMPYKSGV 610
Db 578 GGTGPGASVEHVAENLPCPKGL--PSFRQCCOAHRLSKKGLLAV-----V 627
Oy 611 SPBCKKLCIRANGTYTYVLAAPKYVDGTLSPDSTSYCVGCKIKACDGNLSKKRPD 670
Db 628 VDRKCELYCSPLKESPLVADRVLDTGPGPYETDLGVHGKCKICDGLIGSAKED 687
Oy 671 KGVCGGDNKSCCKVTGFTKPMHGXNFVAIPAGASSIDIRORGYKGLIGDNYLAKN 730
Db 688 RGVCSGSGKCHLVKGFPSH-----ARGTALKDSG-KGST-----N 723
Oy 731 SGGKYLNGHFVSAVERDLVKGSLRYSGTGAVESLQASRPILPELTYEVL-----S 785
Db 724 SDWKLELGEFOIA-----GTTYRYVRNG-LMEKISAKGPKLPLHLMLVLFHDQD 773
Oy 786 VGKMPRPVRYSYLKPKEPRDKSHPKDPR-----GTSV----- 820
Db 774 YG-----IHEYTYVVRNTAENDESEPKPODSLFIWTHSGWEGSGCGGERTIYSC 827
Oy 821 --LHNSVLSLNOVEOPDPRP-----ARVAVGWSGPCSASCGSSGLOKRAYD 865
Db 828 TRIVKKTITLVNDSDCCPASRPPEQVRCNHLPCOSKRVAVAPMPCSCATCEKQOHRVY 887
Oy 866 C---RGSAGRTVPACDAHRPVETOAC-GEPC-PTWELSAMSPCSKGRGFORSIK 919
Db 888 CVYOLQNGTHVATRPVLYCPGPRPAVQSCGQDCISIWESMSQSCSGKGVWKRTVA 947
Oy 920 CVHGRGLIARDQCNLHKRPDLDFC 945
Db 948 CTNSOGK-----CDASTRPRAERAC 967

RESULT 8
O9VF61 PRELIMINARY; PRT; 1229 AA.

AC 09VF61;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CG6107 protein.
GN CG6107.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck K.J., Brinkstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegawa C.,
RA Jaitel M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveit J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003709; AAF55199.1; -.
DR FlyBase; FBgn0038340; CG6107.
DR InterPro; IPR002870; pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR000884; TSPL.
DR InterPro; IPR000130; Zn_MTPetase.
DR Pfam; PF01562; pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR Pfam; PF00090; tsp_1; 2.
DR SMART; SM00209; tsp1; 3.
DR PROSITE; PSS0215; ADAM_MERO; 2.
DR PROSITE; PSS0092; TSP1_2.
DR PROSITE; PSS0142; ZINC_PROTEASE; 1.
DR Hydrolase; Metalloprotease; Zinc.
SQ SEQUENCE 1229 AA; 138136 MW; C1293180AB19B700 CRC64;

Query Match 23.4%; Score 1206.5; DB 5; Length 1229;
Best Local Similarity 32.0%; Pred. No. 4.2e-91;
Matches 321; Conservative 140; Mismatches 329; Indels 213; Gaps 43;

Oy 55 FOITAFQEDFEYLIHTPDQFLAPAFSTEHLGVPLQ-----LTGSSDLRR--CFYSGD 106
Db 195 YNLNVFQRQLHLVLRQDASTV--HNHSMTHIRLKEGSEHGPCRELAERDRLHLCGFSG 253
Oy 107 VNAEPDSFAVSLCGLRGAFYGRGAETVSLPDPNASP-----AAORNSOGAHLQ 158
Db 254 VEDDPHSMVSVSLCGGWTGKTSFGALLIOPVVRTSSDEVLRHVRFSKORNAR--HAYS 311
Oy 159 RRGVPGSPGSDPRTSRGCVASGMNAILRALDPYPRRAGCE-----GSRRRSGRAKRFV 214
Db 312 KFEI-----GLDDEFSKLEQVOEEBOKSKRLKKRHYA 347
Oy 215 SIPIRYV--ETIVVADESQVKEFHGADLEHLLTTLATARLYRHSPTLNPINIVVVL 271
Db 348 DVDNQVYTLLEVLAIVNDMSQFHEDDQPIITLIMSVISIFADASIGNIRILVRLIS 407
Oy 272 LRDRDSQPKV--TGNAALTLRNFCAWQKRLNKVSDKHREYWDPTALLTRQDLGAT-- 325
Db 408 L-----PNINDQTHSSEMLKHKPCG--INGSYER-----DTAMLITREPIGSGVPGK 454
Oy 326 TCDTLGADVGTMCDPKRSQSVIEDDGLPSAFTTAHGLGVFWMPHDNVKVCSEVGGKLR 365

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Db 903 PLENNOSKAPBPLFMWHTSMEDCDATCGGGERKTTVCTKIMSKNISIVNECKXYLT 962
OY 830 ---NOVEQDDRR-PAWVAGSWGPCASGSGLOKRAVDCRSAGORVPAD-----AA 881
Db 963 KPEPOIRKNEQOCQOTRMWTEMTWPCSRFCGKMSORVACTOOLNGTLIRAREDCIG 1022
OY 882 HRFVEVQAC-GEPCPT-WELSAWSPCSKSGRGFORSLKCVGHGRLARADCNLHRKP 939
Db 1023 PKRASQOREGOCMTWEGVWSEFSVCKGKIRHRYACTN-----PRKCVLSTRP 1076
OY 940 QELDFC 945
Db 1077 REAEDC 1082

RESULT 11
O8TXS8
ID Q8MXS8 PRELIMINARY; PRT; 1223 AA.
AC Q8MXS8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE A disintegrin-like and metalloprotease with thrombospondin type 1
DE motif 14 precursor.
GN ADAMTS14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21638061; PubMed-11779638;
RA Bolt H., Ramirez A., von Bredelow B., Kubisch C.;
RA "Characterization of ADAMTS14, a novel member of the ADAMTS
RA metalloprotease family";
RA Blochim. Biophys. Acta 1522:221-225(2001).
RT EMBL; AF358666; AAL40229.1;
DR InterPro: IPR002870; Rep_M12B_Proprep.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF01562; Rep_M12B_Proprep; 1.
DR Pfam: PF01421; Repolysin; 1.
DR Pfam: PF00900; TSP_1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00092; TSP1; 1.
KW Signal; Integrin; Protease; Metalloprotease.
FT SIGNAL 1 22
FT SEQUENCE 1223 AA; 13871 MW; 36394ACAD92F170F CRC64;

Query Match 21.7%; Score 1122; DB 4; Length 1223;
Best local similarity 29.9%; Pred. No. 4.4e-84;
Matches 306; Conservative 122; Mismatches 379; Indels 216; Gaps 40;

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OY 331 GNADVTCMDPKRSCSVIEDDGLPSAFTTAHELGHVFNPHD---NVKCEEVGKLIRAN 387
Db 368 GYAPVYGMCHPLRSCALNHEDGSSAFVIAHEGHVGHGHDGAGCADETLGSG---- 423
OY 388 HNSPTLIQIDRANPWSACSAAITDFLDGSHDCLLDPSKPI-SLPEDLPASVTL50 446
Db 424 -VVAFLVQAQAFHFMHSRCSKLELSRYLPS-YDCLLDPEFDPAWQPPRLPGINYSME 480
OY 447 QCELAGVGSKPC---PYMOYCTKLMTGKAKQOMVCOTRHFPWAGTSCGEEKLCLKA 503
Db 481 QCRFDESGYOTCLAEFRTEPCQWLCS-HPDNYPCKTKKGPRLDETCAPKMGFKGH 539
OY 504 CYERHMLINKHRYDGSNAKMDPYPCSRTCGGGYQLARRQCTNTPANGKCYGCVARKYR 563
Db 540 CIKSPEDQYIGDGGWSSWTKFSGCSRSCGGVRSRSCNNPSPAYGGRPLGPRMEYQ 599
OY 564 SCNLEPCPSSASGSKFREDCGAEFNGY-----NHSTNRLTLAVAVPKYSVSPRDKC 617
Db 600 VCNSECPGY--EDFRAQCAKRNXYVHQNAKS-----WVP-YEPDDAQKCE 647
OY 618 LIRANGTGYFYLLARKVYDGLCS-PDSTSVGVGKCIKAGCDNLGSKKRPDKGVCG 676
Db 648 LICQSDATGDNVEMNOVYHDGTCSTYRDYSCARGCVGVGDKVEGSKKADKCGVCG 707
OY 677 GDNKSKKYTGLETK--PMHGYNFVAIPAGASSIDIRGRYGLTGDDNYLAKNS-QG 733
Db 708 GDNHCRVYAGTIGKASKGALKIVIPAGAHIO-----EALKSPRIYVKNQVYG 762
OY 734 KYLLN--GHFVGAVERDLVYKGSLLRYSGTGAVESLQASRPILEPLVYEVLSVGKMP 791
Db 763 SFILNRGK--EATSKTFAMG-LWEWDAVEDAKESLTKSGPLPEALIAL----- 811
OY 792 PRVRYSPFLKEPREDKSSHPRDGRPS-----VLEHNSVLSL--SNQY--EOPDRRP 840
Db 812 -----PRTEGPRSSLAKYIHEDLPLIGSNVLEEMD---T 848
OY 841 ARWVAGSWGPCASGSGLOKRAVDCR----- 867
Db 849 YEMALSKSWAPCSKACGGGIGFTKYGCRRRDHIMVGNHLCDHKKRPKPIRRRCNQHPSCQ 908
OY 868 -----GSAGRT-----VPACDAHNPVETQAC-----EPC 894
Db 909 PWWTEEMGACSRSCGLGVOTRGICQLPLSLNGTHVMPAKACAGDRPARRPLRVPC 968
OY 895 PT-WELSAWSPCSKSGRGFORSLK-----VGHGRLARQCULHKKPOLDRCVL 947
Db 969 PAQWRIGAMSGSATGEGIQQRQVVCRTNANSLGH-----CGDR-PTVQVCSL 1018
OY 948 RPC 950
Db 1019 PAC 1021

RESULT 12
O8TEY8
ID O8TEY8 PRELIMINARY; PRT; 1159 AA.
AC O8TEY8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
GN ADAMTS14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21839041; PubMed-11741898;
RA Colige A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,
RA Li S.W., Prockop D.J., Lapiere C.M., Nusgens B.V.;
RA "Cloning and Characterization of ADAMTS-14, a Novel ADAMTS Displaying

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DB 540 CWMKSPEDQYGGDGGWSSWTKFCSCSGGVRSSRSCNNPSPAYGGFPCGPMFEYQ 599
564 SCNLEPCSPSASAKSFREOCEAFNGY-----NHSTNLTLLAVAVPYSGVSPRDC 617
600 VCNSECCPEPTY--EDFRAQCCAKRNSYYVHQAHS-----WVP--YEPDDAKQCE 647
618 LICRANGTGYFYVLAKVVDGTLCS--PDSTSVCGCKJAKCGDNIGSKRFRDCGVC 676
648 LICGASDITDGYFMNOVHDGTRCSYRDYSVARCECVPGCGDEKVGSKADKCGVC 707
677 GDNKCKKVTGLETK--PMHGYNFVAIPAGASSIDIRQGYKGLIGDDNYALKNS--QG 733
708 GDNHCRRTVYGLGKASKAGALKLVOIPAGARIQI-----EALCKSPHRIYVKKQVYG 762
DB 734 KYLLN--GHFVVSADRDVVKSLRISGTGAVESLQASRPILEPLVEVSVCKMP 791
763 SFLNPKKGK---EATSRFTTAMG--LEMEDAVEDAKESLKTSGPLPELIALAL----- 811
DB 792 PRVYSFYLPKEPREDKSSHHPKDRGPS-----VLHNSVLSL--SNQY--EQPDDRP 840
812 -----PRTEGPRSLAKYVYIHEDLPLISNNVLEEMD---T 848
DB 841 ARVAVGSMGFCASGSGGLQKRAVDGR----- 867
849 YEMALSMAPSCSKACGGGIFETKYGCRRRRDHMHVHRLCDHKRKPPIRRSNQHPCSQ 908
DB 868 -----GSAGORT-----VPACDAHRPVETOAG-----EPC 894
909 PAVVATEMGACSRSYKLGVTGRIQCLPLSLNGTHVMAKACAGDRPARPCLRYPC 968
DB 895 PT--WELSAWSPSCSKSGRGFORSLK-----VGHGGLLARDQCNLHRKPOLDFCVL 947
969 PAQMRIGAMSGCATGEGEIQGQVYVCRTNANSLGH-----CEGDR--PTVQVCSL 1018
DB 948 RPC 950
DB 1019 PAC 1021

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RESULT 14  
096L37 PRELIMINARY; PRT; 1427 AA.

AC 096L37;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Von Willebrand factor-cleaving protease precursor.  
GN ADAMTS13.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN 11)  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX PubMed=11557746;  
RA Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,  
Fujikawa K.;  
RT Structure of von Willebrand factor-cleaving protease (ADAMTS13), a  
RT Metalloprotease Involved in Thrombotic Thrombocytopenic Purpura.;  
RL J. Biol. Chem. 276:41059-41063(2001).  
DR EMBL: AY055376; AAL17652.1; -.  
DR MEROPS: M12.241; -.  
DR InterPro: IPR001580; Reprolysin.  
DR InterPro: IPR000884; TSPL.  
DR InterPro: IPR00130; Zn\_MTPeptide.  
DR Pfam: PF01421; Reprolysin; 1.  
DR Pfam: PF00090; tsp\_1; 4.  
DR PROSITE: PS50215; ADAM\_MERPRO; 1.  
DR PROSITE: PS50092; TSPL; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Protease; Signal.

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FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE.
SQ SEQUENCE 1427 AA; 153632 MW; EB1BC3AABCI4442 CRC64;
Query Match 17.3%; Score 893.5; DB 4; Length 1427;
Best local similarity 29.2%; Pred. No. 5,7e-65;
Matches 250; Conservative 108; Mismatches 347; Indels 151; Gaps 34;
DB 174 CGVAVG--WNP-----ALTRALDPY-----KPRRAGFGESSRRSRGRAPK 213
21 CGFLLCWGRSHNFQOGLQALEPQAVSYLSPAPLKGRRPSGFRQROKOR-----RA 75
DB 214 VSIPIRYETLVVADESMVRFEGADLEHYLLTLATARLYRHPSILNPINIVYKVLNR 273
76 AGGILHELLELVAGPDVFOAHQEDTEREYVLTNINIGALLRDSPLGAFVHLVKKVILL 135
DB 274 DRDSGRKYVGNALTLRNFCAMQKLINKYSDKRPYWDAILFTRODL--CGATTCDTLGM 332
136 EPEGAPNITANLTSLSLVCGMSQTIINPEDDTPGHADLVLYTRDLELPDGNROVRY 195
DB 333 ADVGTMCDEPKRSCSVIEDGLPSAFTTAHELGHVFNPHDNVAVCEVEFGKLRANHMSP 392
196 TOLGACSPWMSCLITIEDTDFDGLVITAHETIGHSFGLHNGARGS-----CGPSGHVMA 251
DB 393 TLIQIDRANP-----WSACSAALITDFLDSGHDCCLD---QSPKPISLPELPGASYT 443
252 -----DGAAPRAGLAWSPCSRRLLSLSAGRARCVWDPDPQSGAGHPDPAQGLYYS 306
DB 444 LSOQCELRVGVSKPCPY-----WQYCTKLCTKAKAGQWVCQRIHPMDGTSGEGKLC 439
307 ANDCRAVAGPRKAVACTFAREHIDMCALSHTPDLOSSSRLLVPLDGTGCGVKKWC 366
DB 500 LKGCAYERHNLNK--HRYDGSMAKMDPYGCSRFGGQVQIARRQCTNPFPANGKCEGV 558
367 SKGRCSIVELTPITIAVHGMSSMGSRSPCSRSGGCVYVTRRQCNPRAPFGGRACVGA 426
DB 559 RVKYSQNLKPPCSSASGSKFREOCEAFNG-----YHSTNLTLLAVAV--V 604
427 DLQEMKNTQACEKTO--LEFMSQCARTDGQPLRSSPGGASFYH-----MGAAY 474
DB 605 PKTSGVSPRDKCLICRANGTGYFYVLAKPVVGTILCS-----DST--SVCYGCKIKAG 658
475 PHSQGA--LCRHMCRAIGESFTIMRGDSFLDGTICMPGPREDDGLSLCVSGSCRTFG 531
DB 659 CDGNLGSKRREDFCGVCGGDNKCKKVTGLETK--KPMHGYNFVAIPAGASSIDIRQGY 716
532 CDGRMSQVWMDKCYCGGDNSTCSRKGSFTAGRAEYVTFLYTP--NLTSYI--ANH 588
DB 717 KGLIGDNYLALKNSQKYLNGHFVVS--AVERDLVVKSL--LRYSGTGAVESLQASR 773
589 RPLF---THLAVRIG--GRVYVAKMSISPTTYPSLLEDGRVEYRVALLTDRLPLEEIR 644
DB 774 ---PILEPLVEYL-----SVGKMTPRVRYSTYLRKPREDEKSSHHPKDRGPSVLHNSV 825
645 IWPGLQEDADIDIVRYRGEYGNLTRDITFTYFQPK----- 681
DB 826 LSLSNQVEQDDPPARKV--AGSMGSPSASGSGLOKRAVDCGSAGQRTVPA--CDAH 882
682 -----PROAMVVAAYRGPSCVSCGAGLRVAVNSCLDQAKELVETVYCGGSGQ 728
DB 883 R-EVETQAGC--EPCPT--WELSAWSPSCSKSGRGFORSLKCVGHGRLT-----ARDQCN 934
729 QPAPWPEACVLEPCQPYWAVAGDFGPGSASGGGLRERPVACVEAGSLTLTPPARCAG 788
DB 935 LHRKPOLDFCVLRPC 950
DB 789 AQPAPVALTCNPOPC 804

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RESULT 15  
09GL54 PRELIMINARY; PRT; 269 AA.  
ID 09GL54  
AC 09GL54;



GenCore version 5.1.4 p5\_4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 17:12:21 ; Search time 21.1175 Seconds

(without alignments)  
3604.758 Million cell updates/sec

Title: US-10-009-332-1

Perfect score: 5164  
Sequence: 1 MLLGLITLAFAGRTAGPFE.....DQCNIHRKPFQELDFCLRPC 950

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_Aa:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP:\*

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13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP:\*

14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB\_PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5156	99.8	950	10 US-09-965-631-4	Sequence 4, Appl
2	4242.5	82.2	833	9 US-10-163-316-2	Sequence 2, Appl
3	2482.5	48.1	950	10 US-09-321-987B-4	Sequence 4, Appl
4	2482.5	48.1	968	9 US-10-163-316-7	Sequence 7, Appl
5	2480.5	44.0	967	12 US-10-105-929-2	Sequence 2, Appl
6	2274	44.0	727	9 US-10-097-597-1	Sequence 1, Appl
7	2274	44.0	727	9 US-10-097-580-1	Sequence 1, Appl
8	2274	44.0	727	10 US-09-445-023A-1	Sequence 1, Appl
9	2273	44.0	727	9 US-10-097-597-12	Sequence 12, Appl
10	2273	44.0	727	10 US-09-445-023A-12	Sequence 12, Appl
11	2213	40.9	905	10 US-09-918-171A-9	Sequence 9, Appl
12	2113	40.9	1629	10 US-09-972-467-2	Sequence 2, Appl
13	1965	37.1	837	9 US-10-174-590-352	Sequence 352, App
14	1916	37.1	837	9 US-10-176-758-352	Sequence 352, App
15	1916	37.1	837	9 US-10-176-737-352	Sequence 352, App
16	1916	37.1	837	9 US-10-173-706-352	Sequence 352, App
17	1916	37.1	837	9 US-10-173-738-352	Sequence 352, App
18	1916	37.1	837	9 US-10-175-752-352	Sequence 352, App
19	1916	37.1	837	9 US-10-175-752-352	Sequence 352, App

20	1916	37.1	837	9	US-10-176-482-352	Sequence 352, App
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25	1916	37.1	837	9	US-10-174-572-352	Sequence 352, App
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37	1916	37.1	837	9	US-10-176-985-352	Sequence 352, App
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39	1916	37.1	837	9	US-10-176-991-352	Sequence 352, App
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#### ALIGNMENTS

9, 29, 200

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; Sequence 4, Application US/09965631																					
; Patent No. US20020115842A1																					
; GENERAL INFORMATION:																					
; APPLICANT: Fiddle, Carl Johan																					
; APPLICANT: Hibun, Erin																					
; TITLE OF INVENTION: NO. US20020115842A1 Human Proteases and Polynucleotides Enc																					
; FILE REFERENCE: LEX-0241-USA																					
; CURRENT APPLICATION NUMBER: US/09/965,631																					
; CURRENT FILING DATE: 2001-09-27																					
; PRIOR APPLICATION NUMBER: US 60/236,689																					
; PRIOR FILING DATE: 2000-09-29																					
; SOFTWARE: FastSeq for Windows Version 4.0																					
; NUMBER OF SEQ ID NOS: 7																					
; SEQ ID NO 4																					
; LENGTH: 950																					
; TYPE: PRT																					
; ORGANISM: homo sapiens																					
US-09-965-631-4																					
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Best Local Similarity 99.8%; Score 5156; DB 10; Length 950;																					
Matches 949; Conservative 0; Mismatches 1; Indels 0; Gaps 0;																					
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DB	1	MLLGLITLAFAGRTAGPFE	REVVVP	RI	LD	PD	IN	GR	RY	WR	GP	ED	SG	DG	LI	FO	IT	AF	60		
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QY	181	NPATLRALDEYKPRRA	FG	ES	RS	RR	SG	RA	KRF	VS	IP	RY	VE	TL	LV	AD	ES	HW	KF	GA	240
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DB	181	NPATLRALDEYKPRRA	FG	ES	RS	RR	SG	RA	KRF	VS	IP	RY	VE	TL	LV	AD	ES	HW	KF	GA	240
QY	241	YLLTLLTAARLRVHP	SI	LN	P	IN	I	V	Y	K	V	L	L	R	D	S	G	P	K	Y	300
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DB	241	YLLTLLTAARLRVHP	SI	LN	P	IN	I	V	Y	K	V	L	L	R	D	S	G	P	K	Y	300

9, 29, 2000



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Db 241 YLTLTAAARLYRHPSTLNPINIVVAVLLLRDSDSPKVTGNALTLRNCAMOKKLN 300
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OY 901 AWSPCSCKGCGFQRRSLKCVGHGRLARDOCNLHRRKPEQLDFCVLRPC 950
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RESULT 2  
US-10-163-316-2

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: Sequence 2, Application US/10163316
: Publication No. US20020197703A1
: GENERAL INFORMATION:
: APPLICANT: Kapellier-Libermann, Rosana
: TITLE OF INVENTION: 65557, A Human Matrix Metalloproteinase and Uses
: TITLE OF INVENTION: Therefor
: FILE REFERENCE: MPI01-025PIRM
: CURRENT APPLICATION NUMBER: US/10/163,316
: CURRENT FILING DATE: 2002-06-05
: PRIOR APPLICATION NUMBER: 60/297,863
: PRIOR FILING DATE: 2001-06-13
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 823
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-163-316-2

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Query Match 82.2%; Score 4242.5; DB 9; Length 823;  
Best Local Similarity 96.9%; Pred. No. 5.5e-295;  
Matches 791; Conservative 0; Mismatches 2; Indels 23; Gaps 1;

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Db 1 MLLGILTLAPAGTAGGEPEEREVYVPIRLDPDINGRRYYWRGEDSGDGLFQITAF 60
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Db 61 QEDFLHTLPDQOFLAPAFSTEHGLVPLQGLTGSSDLRCFYSQDVAAEDSPFAVSLC 120
OY 121 GGLRCAGFYRGAEVYISPLPNASAPAAORNSOAHLLORRVPGPSDDPTSRGVASGW 180
Db 121 GGLRCAGFYRGAEVYISPLPNASAPAAORNSOAHLLORRVPGPSDDPTSRGVASGW 180
OY 181 NPAILRALDPYKPRRAGGESRRRSRGRARFVSIPIRYETLVVADESMVKFHGADLEH 240
Db 181 NPAILRALDPYKPRRAGGESRRRSRGRARFVSIPIRYETLVVADESMVKFHGADLEH 240
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Db 241 YLTLTAAARLYRHPSTLNPINIVVAVLLLRDSDSPKVTGNALTLRNCAMOKKLN 300
OY 301 KVSDEHPYMTAILFTRODLCGATTCDTLGMADVGTMCDPKRSQVIEDGLPSAFTTA 360
Db 301 KVSDEHPYMTAILFTRODLCGATTCDTLGMADVGTMCDPKRSQVIEDGLPSAFTTA 360
OY 361 HELGHVFNMPHDNVKVEVEFGKLRANHMSPPTLIQIDRANPWSACSAIITDFLDSG 420
Db 361 HELGHVFNMPHDNVKVEVEFGKLRANHMSPPTLIQIDRANPWSACSAIITDFLDSG 420
OY 421 DCLLDQPSKPISTLPEDLFGASTYLSQCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
Db 421 DCLLDQPSKPISTLPEDLFGASTYLSQCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
OY 481 QTRHPMADGTSCGEGKCLTGACACVERHNLMKHR-----VDG 517
Db 481 QTRHPMADGTSCGEGKCLTGACACVERHNLMKHRPTDIISPKQLLRPLRGHLHTQYDG 540
OY 518 SMAKMDPYGPCSRGCGGVOLARROCTNPFPANGKCEGVRYKSCNLEPCPSASGK 577
Db 518 SMAKMDPYGPCSRGCGGVOLARROCTNPFPANGKCEGVRYKSCNLEPCPSASGK 577
OY 578 SFREBOCEAFNGYNHSTRLTLA VAWPKYSGVSPRDKCKLICRANGTYVLA PKVVD 637
Db 578 SFREBOCEAFNGYNHSTRLTLA VAWPKYSGVSPRDKCKLICRANGTYVLA PKVVD 637
OY 601 GNLGSKRRFDCGVCVGDNKCKKVTGTFKPMHGYN 660
Db 601 GNLGSKRRFDCGVCVGDNKCKKVTGTFKPMHGYN 660
OY 638 GTLCSPDSTSVGVGKCIKACDGNLGSKRRFDCGVCVGDNKCKKVTGTFKPMHGYN 720
Db 638 GTLCSPDSTSVGVGKCIKACDGNLGSKRRFDCGVCVGDNKCKKVTGTFKPMHGYN 720
OY 698 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVSAVERDLVYKGSLL 757
Db 698 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVSAVERDLVYKGSLL 757
OY 721 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVSAVERDLVYKGSLL 780
Db 721 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVSAVERDLVYKGSLL 780
OY 758 RYSGTGRAVESLQASRPILPELTVEVLTVGKMPRP 793
Db 758 RYSGTGRAVESLQASRPILPELTVEVLTVGKMPRP 816

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RESULT 3  
US-09-321-987B-4

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: Sequence 4, Application US/09321987B
: Patent No. US20020102210A1
: GENERAL INFORMATION:
: APPLICANT: Kimble, Judith E
: APPLICANT: Bielloch, Robert H
: TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
: FILE REFERENCE: 960296,95386
: CURRENT APPLICATION NUMBER: US/09/321,987B
: CURRENT FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/087,170
: PRIOR FILING DATE: 1998-05-29
: PRIOR APPLICATION NUMBER: 60/129,023
: PRIOR FILING DATE: 1999-04-13
: NUMBER OF SEQ ID NOS: 5

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Db	603	RVRIRSCNIEECPPDN-NKOTFREOCQAHNEFSAASGNEPYEWTPKTIAGVSEPKDRCKL	661
QY	619	ICRANGTCYFYVLA PKVVDGTGLCSBDSTSVYOGKCIACACDGNLGSKKRFRKQYVCGD	678
Db	662	TCEKAGLIEFYFVLQPKVVDGTPCSPBDSTSVYOGQCYKACADRIIDSKKKFRKQYVCGN	721
QY	679	NKSKCKVYGLGTRKMHGYNFVVALIPASSSIDIMQREYIKGLIGDNTLAKNSOQKYL N	738
Db	722	GSTCKKMSGIYTSRPGIHDVTLIPACATINLEVAHNRKOSRRNNGSLAIRADGTYIL N	761
QY	739	GHPVVASAVERDLVYKGSILRYSGTGTAVESIOASRPILDEULTEVIVSVGKMPRYVYSF	798
Db	782	GNFTLSTLEODLTQYKGVYLRISGSSALDERLRSPSLKEPDLITQVLA VGHALPKIKFY	841
QY*	799	YLPEPRERDKSHHKDRGSEVILNLSVLSNOVEQEDDPPRPAWVAGSNGPCASCGSG	858
Db	842	FMKKRTES-----FNALPTES-----EWTLEEMGECSKTCGSG	874
QY	859	LQKRAVVDGSGSAGORTVPACDAAH--RPVETOAGE-PCPTWELSAVSPCSKGRGROF	915
Db	*875	WQRYVQOCRODINGH---PASCAEAIVAPASTRPACDLPCPHMVGYDMSPCSKCGKGYK	931
QY	916	RSLKCVGHGGRLLARDQCNLHRRQOE-LDPCLVAPC	950
Db	932	RTLKCVSHDGVLINSESCDPLKRAKRYHIDCCTLQOC	967

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RESULT 5
US-10-105-929-2
Sequence 2, Application US/10105929
Patent No. US20020137142A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/10/105,929
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 967
TYPE: PRT
ORGANISM: Homo sapiens
US-10-105-929-2

```

Query Match	48.0%;	Score 2480.5;	DB 12;	Length 967;
Best Local Similarity	48.9%;	Pred. No.5.7e-169;		
Matches 485;	Conservative 154;	Mismatches 251;	Indels 101;	Gaps 24

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QY 1 MLIIIGLITLFAAGSTAGGAFEEPERVWPIRIDPDINRRYRWSPEDSGOGLFOTLA 60
    |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 36 ILLIAAALLIIVSDMLGRPSDEDELIYV-ELE-----RAV---GHCTTRLRHAF 81

QY 61 QEDFYHLHTPDPAQFLAPAFSTEHLG-----VPLQGLTGSSSDLRRCFYSGDVAAEDSF 114
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 82 DQGLDELTRPDSPSELAGFTLQNGRKSGETPLP-----ETDLAHCFYSGTVNGDPSA 136

QY 115 AAVSLCGSLKGAFETYRCRAEVIYISLPNAS---APAQRNSOGA---HLIQ---RGVPG 165
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 137 AALSICGVRCAFAFLIGEAFFIOLPLASERLTAAGAEGKPPAPLOFHLIRRNQGVGC 196

QY 166 PSG-----DPTSRC-----GYASG---NMPALIRLMDPKPRRPAFGESRSRRS 207
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 197 TCGVADDEPRPTGAETFEDEDECTEGSDEBPWS-----PDPAIAGVGQ-ITGGS 247

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QY	208	GRKRFVSI	PRVYELVYVAD	SMYKFRGAD	LEHLLLL	LLTAARL	YHNS	PLIN	IVVY	267																																														
Db	248	IRKKRFVS	HRVYELVYVAD	SMAEFH	SGSK	AKHYLL	LD	FVAALY	KHPS	IRNSV	SLVY	3077																																												
QY	268	KVLL	RDSDSG	PKYTG	NAL	LF	NFC	AMOK	LK	LVSP	KHPE	WYOTAL	LF	ROD	CGATT	3277																																								
Db	308	KILV	HDQK	PEV	T	SNAL	LL	RF	CM	OKO	HN	PP	SR	DA	EH	DTALL	LF	ROD	CGSQC	3677																																				
QY	328	DTL	GADV	GT	CM	DR	PC	RS	CS	YIED	DL	PS	AF	TT	HA	EL	GV	NM	PD	NK	YCE	EV	FK	LRAN	3877																															
Db	368	DTL	GADV	GT	CD	PS	RS	CS	YIED	DL	QA	FT	TA	HE	L	GV	NM	PD	AK	Q	AS	L	NG	VQ	DS	4277																														
QY	388	HM	ST	L	I	Q	D	R	A	N	P	M	S	A	C	S	A	I	T	T	D	L	S	H	G	C	L	L	D	O	S	K	P	T	S	P	E	D	I	P	G	A	S	T	L	S	O	4477								
Db	428	HM	M	S	M	L	N	D	I	S	O	P	S	P	C	S	A	M	T	T	S	F	L	D	N	H	G	E	L	M	D	K	P	O	N	P	T	O	L	P	E	D	I	P	G	T	S	D	A	N	4877					
QY	448	C	E	L	A	N	G	V	S	K	P	C	P	-	Y	M	O	Y	C	T	K	M	O	T	G	A	K	O	M	O	Y	O	T	H	R	P	A	B	O	T	S	G	E	E	K	L	K	A	C	Y	5067					
Db	488	C	O	F	T	F	E	D	S	K	P	D	A	S	T	C	S	T	M	O	T	G	S	G	L	V	Y	O	T	H	R	P	A	B	O	T	S	G	E	E	K	M	C	L	N	G	A	V	N	5477						
QY	507	R	H	N	L	N	K	-	-	-	R	V	D	S	M	A	K	M	P	E	Y	G	P	C	S	R	T	G	O	G	G	Y	O	L	A	R	O	C	T	N	P	P	A	N	G	R	K	Y	C	E	G	V	R	K	Y	5537
Db	548	K	T	D	-	R	K	H	E	D	P	F	H	S	G	M	G	M	G	P	M	D	C	S	R	T	G	G	G	Y	T	M	R	E	C	D	N	P	P	K	N	G	K	Y	C	E	G	K	R	Y	R	6067				
QY	564	S	C	N	L	E	P	C	S	S	A	S	G	S	F	R	E	O	C	E	A	N	G	N	H	S	T	N	L	L	T	A	V	A	M	P	K	S	G	V	S	P	R	D	C	K	L	I	C	R	A	N	6237			
Db	607	S	C	N	L	E	D	C	P	D	-	N	G	K	T	F	R	E	O	C	E	A	N	E	R	S	K	A	S	F	G	S	P	A	V	E	M	I	P	K	A	G	S	P	R	D	R	O	K	L	I	C	O	A	K	6657
QY	624	G	T	G	F	E	Y	L	A	P	K	Y	O	G	T	C	S	P	S	T	E	V	C	O	G	A	K	I	R	K	G	C	O	G	N	L	S	K	R	F	P	C	S	C	V	G	G	A	D	N	S	C	K	6837		
Db	666	G	I	G	F	E	Y	L	O	P	K	Y	O	G	T	C	S	P	S	T	E	V	C	O	G	A	K	D	R	I	I	D	S	K	K	P	F	K	C	V	G	C	O	G	N	S	T	C	K	7257						
QY	684	K	V	T	G	L	F	T	P	M	H	G	Y	N	V	A	I	P	A	G	A	S	I	D	I	R	O	R	K	Y	G	L	I	G	D	N	I	A	L	K	N	S	O	G	K	Y	L	L	N	G	H	E	V	Y	7437	
Db	726	K	I	S	G	V	T	S	A	K	G	Y	H	D	I	T	I	P	G	A	N	I	E	V	O	K	O	R	N	O	G	S	R</																							

RESULT 6  
 US-10-097-597-1  
 ; Sequence 1, Application US/10097597  
 ; Publication No. US20030022352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hirose, Kunitaka  
 ; APPLICANT: Inoguchi, Eiji  
 ; APPLICANT: Hakozaaki, Michinori  
 ; APPLICANT: Ishioka, Keiko  
 ; APPLICANT: Ishida, Yukako  
 ; APPLICANT: Matsushima, Kouji  
 ; APPLICANT: Kuno, Kouji  
 ; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,  
 ; TITLE OF INVENTION: pharmaceutical  
 ; FILE REFERENCE: 057092  
 ; CURRENT APPLICATION NUMBER: US/10/097,597  
 ; CURRENT FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: 09/445,023  
 ; PRIOR FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: JP 9-160422  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1  
 LENGTH: 727  
 TYPE: PRF  
 ORGANISM: Homo sapiens  
 US-10-097-597-1

Query Match 44.0%; Score 2274; DB 9; Length 727;  
 Best Local Similarity 54.4%; Pred. No. 2.2e-154;  
 Matches 408; Conservative 129; Mismatches 173; Indels 40; Gaps 11;

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OY 209 RAKRVSIPRYETLVANDESVMKFGADLEHYLLTLATARLYRHPISLIPINIVYVK 268
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DB 9 RKKRVSSPRVETLVADQSAEFGSLKHYLLTLFSVARKLKHBSIRSVSLVYVK 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 269 VLLLRDSDGPKVYTNALTLRNFCAWOKLNVSDKHREYDITLFTRODLGATTCO 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 ILVIHDEQKGPVETSNALTLRNFCAWOKLNVSDKHREYDITLFTRODLGATTCO 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 329 TLGMADVTGCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKCEEFGLKLRANH 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 129 TLGMADVTGCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKCEEFGLKLRANH 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 389 MMSPTLIQIDRANPWSASAAITITFDLSDGHDCLLDQPSKPSLPEDLPASVYLSQOC 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 189 MMSASLNLSDHSQWSPSAVITSTFLDNGHECLMDKQNPQLPGLDPLGLYDANRQC 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 449 ELAFVGSKPCP-YMOCYCTKLWCTGKAKGOMYCOTRHPFADGTSCEGLKLGACVYR 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 QFTFEDSKHCDASTCTLMCTGSGVLVLCQTHFPMAGTSCGSECKWICNGCVYK 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 508 HNLNKH--RYDGSNAKMDPYGRCSTCGGVQLARROCTNPTPANGKYYCEGVRYKYS 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 309 TD-RKHFDTPFHGSMGPMGMDCSRTCGGVQYTMRECDNVPKNGKYCEGKRYRYS 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 565 CULECPSSASGKSPRECECAFNQYHNSTNRLTLAVANVPYSGVSPRDKCLICRANG 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 368 CULECPDN-NKTRFEECEAHNEFSKASFGSPRAVEITPKYAGVSPDRCKLICQANG 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 625 TGYFVLAPKVVYDGLTSCPDSTSVCOGCKIRAGCDGNLGSKKRDKCGVCGGDNKSK 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 IGFVFLAPKVVYDGLTSCPDSTSVCOGCKIRAGCDGNLGSKKRDKCGVCGGDNKSK 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 685 VTGLTPKPMHGNFYVALPAGASSIDIRORGYKGLIGDNNYALAKNSOKYLLNGHFVYS 744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 487 IGSVTSAPKGYHDITVITPGATNIEVKORNOGSRNNNSFLAIKADGTYYLNGDYTLLS 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 745 AVERDLVVYGLSLRYSGTAVESLOASRPILPELVEVLSYGKMTPRVRSFYLPKRP 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 547 TLEQDITMYGVLYRYSGSSALERIRSFPLKEPLTIQVLYGNALRPRIKITYFYVKKR- 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 805 REDKSSHPKDPKPGPVYLANSVLSNQVQPDPRPARVAVAGSWGFCASCGSGLOKRAV 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 606 ---KES-----FAIIPTF-----AVIIEWGSCSKSCELGQMRRLV 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 865 DCRGSAQORTVPACDAH--RPEVQAGE-PCPTWELSMSPSCSCRGFORSLKCY 921
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 640 ECRDINGO---PASECAKLVKPASTRPCADHPCPOMQLGEMSSCKTKCKKKRKLCL 696
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 922 GHGGRLLARDQCNLHRRPOE-LDFCVLAPC 950
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 697 SHDGVLSHESCDPLKKPKHFTDFCLTQC 726
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RESULT 7  
 US-10-097-580-1  
 Sequence 1, Application US/10097580  
 Publication No. US20030032168A1  
 GENERAL INFORMATION:  
 APPLICANT: Hirose, Kunitaka

APPLICANT: Inoguchi, Elji  
 APPLICANT: Hakozaaki, Michio  
 APPLICANT: Ishioke, Keiko  
 APPLICANT: Ishida, Yukako  
 APPLICANT: Matsushima, Kouji  
 APPLICANT: Kuno, Kouji  
 TITLE OF INVENTION: Human ADAMS-1 protein, gene encoding the same, pharmaceutical  
 FILE REFERENCE: 057092  
 CURRENT APPLICATION NUMBER: US/10/097,580  
 PRIOR FILING DATE: 2002-03-15  
 PRIOR APPLICATION NUMBER: 09/445,023  
 PRIOR FILING DATE: 1999-12-03  
 PRIOR APPLICATION NUMBER: JP 9-160422  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1  
 LENGTH: 727  
 TYPE: PRF  
 ORGANISM: Homo sapiens  
 US-10-097-580-1

Query Match 44.0%; Score 2274; DB 9; Length 727;  
 Best Local Similarity 54.4%; Pred. No. 2.2e-154;  
 Matches 408; Conservative 129; Mismatches 173; Indels 40; Gaps 11;

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OY 209 RAKRVSIPRYETLVANDESVMKFGADLEHYLLTLATARLYRHPISLIPINIVYVK 268
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DB 9 RKKRVSSPRVETLVADQSAEFGSLKHYLLTLFSVARKLKHBSIRSVSLVYVK 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 269 VLLLRDSDGPKVYTNALTLRNFCAWOKLNVSDKHREYDITLFTRODLGATTCO 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 ILVIHDEQKGPVETSNALTLRNFCAWOKLNVSDKHREYDITLFTRODLGATTCO 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 329 TLGMADVTGCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKCEEFGLKLRANH 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 129 TLGMADVTGCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKCEEFGLKLRANH 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 389 MMSPTLIQIDRANPWSASAAITITFDLSDGHDCLLDQPSKPSLPEDLPASVYLSQOC 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 189 MMSASLNLSDHSQWSPSAVITSTFLDNGHECLMDKQNPQLPGLDPLGLYDANRQC 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 449 ELAFVGSKPCP-YMOCYCTKLWCTGKAKGOMYCOTRHPFADGTSCEGLKLGACVYR 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 QFTFEDSKHCDASTCTLMCTGSGVLVLCQTHFPMAGTSCGSECKWICNGCVYK 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 508 HNLNKH--RYDGSNAKMDPYGRCSTCGGVQLARROCTNPTPANGKYYCEGVRYKYS 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 309 TD-RKHFDTPFHGSMGPMGMDCSRTCGGVQYTMRECDNVPKNGKYCEGKRYRYS 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 565 CULECPSSASGKSPRECECAFNQYHNSTNRLTLAVANVPYSGVSPRDKCLICRANG 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 368 CULECPDN-NKTRFEECEAHNEFSKASFGSPRAVEITPKYAGVSPDRCKLICQANG 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 625 TGYFVLAPKVVYDGLTSCPDSTSVCOGCKIRAGCDGNLGSKKRDKCGVCGGDNKSK 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 IGFVFLAPKVVYDGLTSCPDSTSVCOGCKIRAGCDGNLGSKKRDKCGVCGGDNKSK 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 685 VTGLTPKPMHGNFYVALPAGASSIDIRORGYKGLIGDNNYALAKNSOKYLLNGHFVYS 744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 487 IGSVTSAPKGYHDITVITPGATNIEVKORNOGSRNNNSFLAIKADGTYYLNGDYTLLS 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 745 AVERDLVVYGLSLRYSGTAVESLOASRPILPELVEVLSYGKMTPRVRSFYLPKRP 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 547 TLEQDITMYGVLYRYSGSSALERIRSFPLKEPLTIQVLYGNALRPRIKITYFYVKKR- 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 805 REDKSSHPKDPKPGPVYLANSVLSNQVQPDPRPARVAVAGSWGFCASCGSGLOKRAV 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 606 ---KES-----FAIIPTF-----AVIIEWGSCSKSCELGQMRRLV 639
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OY 865 DCRGSAQORTVPACDAH--RPEVQAGE-PCPTWELSMSPSCSCRGFORSLKCY 921
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 640 ECRDINGO---PASECAKEVPASTRPCADHPQWOLGEMSSCSKTCGKGRKRSIKCL 696  
QY 922 GHGGRLARDQCNLHRRKPOE-IDFCVLRPC 950  
Db 697 SHDGGVLSHESCPLKKPKHFIIDFCTLTQC 726

RESULT 8  
US-09-445-023A-1  
; Sequence 1, Application US/09445023A  
; Patent No. US20020119167A1  
; GENERAL INFORMATION:  
; APPLICANT: Hirose, Kunitaka  
; APPLICANT: Inoguchi, Ei-ji  
; APPLICANT: Hakozaaki, Michinori  
; APPLICANT: Ishioke, Keiko  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Kuno, Kouji  
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
; FILE REFERENCE: 057092  
; CURRENT APPLICATION NUMBER: US/09/445,023A  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: JP 9-160422  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 727  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-445-023A-1

Query Match 44.0%; Score 2274; DB 10; Length 727;  
Best Local Similarity 54.4%; Pred. No. 2, 2e-154;  
Matches 408; Conservative 129; Mismatches 173; Indels 40; Gaps 11;

QY 209 RAKREVSIRPVETLVVADESVMKFRGADLEHLLTLTAARLYHPSILNPINIVYK 268  
Db 9 RKRREVSIRPVETLVVADESVMKFRGADLEHLLTLTAARLYHPSILNPINIVYK 68  
QY 269 VILLRDRDQPKYTGNAALTLRNFCAWOKLVNSDKHREYWDATLFTRODLCGATTC 328  
Db 69 ILVIEHQKREYTSNAALTLRNFCAWOKLVNSDKHREYWDATLFTRODLCGATTC 128  
QY 329 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHNDYKCEVEFGKLRANH 388  
Db 129 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHNDYKCEVEFGKLRANH 188  
QY 389 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDOPSKTSLPEDLPASATYLSQOC 448  
Db 189 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDOPSKTSLPEDLPASATYLSQOC 248  
QY 449 ELAFVGSRCPC-YMOCYTKLMCTGKAKGOMVOTRHFPADTSCGEGKLCAGACVER 507  
Db 249 QTFEGEDSHCPDAASTCTTLMCTGTSGGLVLCQTKHFPADTSCGEGKLCAGACVER 308  
QY 508 HNLNKH---RVDSMAKMDPYGPCSRTCGGVOLARRCOTNPYPANGKCYCEGVYKRS 564  
Db 309 TD-RKHFDPFPHGSMGPMGPMGDCSRTCGGVOLARRCOTNPYPANGKCYCEGVYKRS 367  
QY 565 CNLEPCPSSASGKSFREOCCEAFNGYHSTNRLTLAVAWPKYSGVSPRDKCLIRANG 624  
Db 368 CNLEPCPSSASGKSFREOCCEAFNGYHSTNRLTLAVAWPKYSGVSPRDKCLIRANG 426  
QY 625 TGFFYLAKRYVDGTLCSPDSTSVYQKCIKACGCGNIGSKRREDKCGVCGGDNKSCCK 684  
Db 427 IGFFFLQKRYVDGTLCSPDSTSVYQKCIKACGCGNIGSKRREDKCGVCGGDNKSCCK 486  
QY 685 VTGLFTKPMHGYVFAVAPAGASSIDIRQKGLIGDNYLALNKSQKYLINGHFFVYS 744  
Db 487 ISSSVTSAPRGHDIYITITGATINIEVKORNGSRNNGSFLAIKADGTYILNGDYTIS 546

QY 745 AVERDLVKGSLARTSGTAVESLOASRPILPELVFVSYGKMPPRYRSPYLKEP 804  
Db 547 TLEDIMIKGVLYKRTSGSALERKNSFPLKEPLTQVLVGAALPKRTIYEVYK 605  
QY 805 REDKSSHPKDRGSPVJHNSVLSLNOVEOPDDRPAPARWAGSWGPCSAGSLORAV 864  
Db 606 ---KES-----FNIPFES-----AWIEMGECSSKSCGELGMORRLV 639  
QY 865 DCRSAGQRTVPACDAH--RPVETQACGE-PCPTWLSMWSRCSGCGFQRRSLKY 921  
Db 640 ECRDINGO---PASECAKEVPASTRPCADHPQWOLGEMSSCSKTCGKGRKRSIKCL 696  
QY 922 GHGGRLARDQCNLHRRKPOE-IDFCVLRPC 950  
Db 697 SHDGGVLSHESCPLKKPKHFIIDFCTLTQC 726

RESULT 9  
US-10-097-597-12  
; Sequence 12, Application US/10097597  
; Publication No. US20030022352A1  
; GENERAL INFORMATION:  
; APPLICANT: Hirose, Kunitaka  
; APPLICANT: Inoguchi, Ei-ji  
; APPLICANT: Hakozaaki, Michinori  
; APPLICANT: Ishioke, Keiko  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Kuno, Kouji  
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,  
; FILE REFERENCE: 057092  
; CURRENT APPLICATION NUMBER: US/10/097,597  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: 09/445,023  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: JP 9-160422  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 727  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-097-597-12

Query Match 44.0%; Score 2273; DB 9; Length 727;  
Best Local Similarity 53.7%; Pred. No. 2, 6e-154;  
Matches 403; Conservative 131; Mismatches 176; Indels 40; Gaps 10;

QY 209 RAKREVSIRPVETLVVADESVMKFRGADLEHLLTLTAARLYHPSILNPINIVYK 268  
Db 9 RKRREVSIRPVETLVVADESVMKFRGADLEHLLTLTAARLYHPSILNPINIVYK 68  
QY 269 VILLRDRDQPKYTGNAALTLRNFCAWOKLVNSDKHREYWDATLFTRODLCGATTC 328  
Db 69 ILVIEHQKREYTSNAALTLRNFCAWOKLVNSDKHREYWDATLFTRODLCGATTC 128  
QY 329 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHNDYKCEVEFGKLRANH 388  
Db 129 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHNDYKCEVEFGKLRANH 188  
QY 389 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDOPSKTSLPEDLPASATYLSQOC 448  
Db 189 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDOPSKTSLPEDLPASATYLSQOC 248  
QY 449 ELAFVGSRCPC-YMOCYTKLMCTGKAKGOMVOTRHFPADTSCGEGKLCAGACVER 507  
Db 249 QTFEGEDSHCPDAASTCTTLMCTGTSGGLVLCQTKHFPADTSCGEGKLCAGACVER 308  
QY 508 HNLNKH---RVDSMAKMDPYGPCSRTCGGVOLARRCOTNPYPANGKCYCEGVYKRS 564

[illegible]

```

RESULT 10
US-10-097-580-12
Sequence 12, Application US/10097580
Publication No. US20030032168A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiji
APPLICANT: Hakozaeki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMS-1 protein, gene encoding the same, pharmaceutical
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 727
TYPE: PRT
ORGANISM: Mus sp.
US-10-097-580-12

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[illegible][illegible]

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US-09-445-023A-12
RESULT 11
US-09-445-023A-12
Sequence 12, Application US/09445023A
Patent No. US20020119167A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiichi
APPLICANT: Hakezaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
FILE REFERENCE: 057092
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS-1
CURRENT FILING DATE: 1999-12-03
CURRENT APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
PRIOR APPLICATION NUMBER: JP 9-160422
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 727
TYPE: prt
ORGANISM: Mus sp.
US-09-445-023A-12

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Query Match	44.08;	Score 2273;	DB 10;	Length 727;
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Best Local Similarity 53.7%; Pred. No. 2.6e-154;  
Matches 403; Conservative 131; Mismatches 176; Indels 40; Gaps 10;

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QY 209 RAKREVISIPRYVELLVNVADESVMKFGADLEHYLLTLATARLYRHSILNPIVYVK 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 RKKRRVSSPRVETMLVADQSMADPHSGSLKHLYLLTLFVSARAFYKHSINSLVYVK 68
QY 269 VLLLRDSDGRVYGNALTLRNCAMOKKLNKYSKDKHPEYDIALTLFTRODLGATTC 328
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 ILVYEEKGGEVYSNALTLRNFCSMOKHNSPSDRPEYDIALTLFTRODLGSHYCD 128
QY 329 TLGMADVCTMCDPKRSCSVIEDDGLPSAFTHAHELGHVFNPHDVKACEYFGLRANH 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 TLGMADVCTCDPSKSCSVIEDDGLQAAFTTAHELGHVFNPHDVKACASLNGVSDSH 188
QY 389 MASPTLIQIDRANPWSACSAIITDFLDGHDCLLDPSKPSISPELDPASYSYLQOC 448
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 LMASLSSLDHSQWSPSCSAVMVTSFLDNGHECLMDKQNPILPSDLPGLVYANQC 248
QY 449 ELARGVSKPCP-YNQYCTKLMCTGKAKGQWVCOYTHFPMADGTSCEGKLCGLKAGCYER 507
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 QFTGEESKHCPCDAASTCTTLMCTGTSGLVCOYTHFPMADGTSCEGKVCVSGKCYNK 308
QY 508 HNLNKH---RYDGSWAKMDPYGCSRTGCGGVOLARQCTPTPANGKCYEGVYVKRS 564
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 TDM-KHFTPYHGSWGPWGDSCRTGCGVQYTMRCNDMPVKNKGKCYEGKRVYRS 367
QY 565 CNLEPCSSASGKSFREOCEAFNGYNHSTNRLTLAVAMVYKSGVSPRDKCLICRANG 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 368 CNIECCPDN-NGKTFREOCEAHNFESKASFGNEPTVEMTKYAGVSKDKCLICEAKG 426
QY 625 TGYTYVLAAPKVVYDGLCPDSTSVYCGKCIKAGCDGMLSKKRPDKCGVCGDNKSGCK 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 IGYFVLIOPKVVYDGPSPDSTSVYCGQCYKAGCDRIIDSKKFKDKCGVCGDNKSGCK 486
QY 685 VTGFETKMHGYNFVVALPAGASSIDIRORGYKGLIGDNTLALKNSGKXLLNHNHYVS 744
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 487 MSGITSTRPQYHDIYVTPAGATINLEVAHNRORSRNNGSFLAIRAAGTYILNKNFLS 546
QY 745 AVERDLVYKSLRYSGTGAVESLQASRPILPEPLVEVLSVGMKTPRVRYSFYLPEP 804
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 TLEDGLYKGYVLRSGSSALERIRSPLEPLTIOVLVGNHARKIKIFTYFMKKKT 606
QY 805 REDKSHKDRGPPSVLHNSVLSNOVEOPDPRPARVAGSWGPGSASGSGLOKRAY 864
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 607 ES-----FNALPTFS-----EMVLEEWECECKTGGSGWQRVYV 639
QY 865 DCRSAGORVPACDAH--RPVEOAGCE-PCPTWELSAKSPCSKSGRFORRSIKCY 921
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 640 QCRDINGH---PASECAKEVKPASTRPCADLPCEPMOVGDWSPCSKTCGKGYKKRTLCV 696
QY 922 GHGRLARQCNLHKKPQE-LDFCVLAPC 950
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 SHDGVLSNESCDPLKKRKHIDFCTLQOC 726

```

RESULT 12  
US-09-918-171A-9  
Sequence 9, Application US/09918171A  
Patent No. US20020110894A1  
GENERAL INFORMATION:  
APPLICANT: Aptec, Suneel  
APPLICANT: Hurstainen, Tiina L.  
APPLICANT: Hirohata, Satoshi  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
FILE REFERENCE: 26473/04193  
CURRENT APPLICATION NUMBER: US/09/918, 171A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/369, 364  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentl Ver. 2.1  
SEQ ID NO 9

LENGTH: 905  
TYPE: PRT  
ORGANISM: Mus musculus ADAMTS-8  
US-09-918-171A-9

Query Match 40.9%; Score 2113; DB 10; Length 905;  
Best Local Similarity 45.5%; Pred. No. 9.5e-143;  
Matches 431; Conservative 148; Mismatches 280; Indels 108; Gaps 24;

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QY 2 LLLGILTL-----AFAGRTAGGFEFEREVVPIRLDPDINGRRYWRGPEDSGDOGL 53
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13 LLLLLDLPPEPLVOCAGAGGTGA--QASLVVPTRL-----PGSASE--L 55
QY 54 IFQITAFQEDFYLIHTPDAQFLAPFSTEHLVPLQIGITGSSDLRCEFSGDVNAEPDS 113
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 AFHLSAFGQGVYLRAPLAPASFLAEFEKLERLG--GSSAAGGEPGLKGFSGTYNGERES 114
QY 114 FAVYSLCGFLGAGCYRGAEEVVISPLPASAAPAAORNSQA-----HILDRGVGCP 166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 115 LAAMSVAGWSGSFLAEERTIOP-----QAGDSLDPQPHRLQRMG-PGQR 160
QY 167 SGDPTSRGVSAGNNPALIRALDYPKPRRAGFSGRS-----RRSG----- 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 REDP-----GLAAEYFPLPQGLEMEVENGGQGERSONEDKKQDKKELKETEDSKY 216
QY 209 -----RAKREVISIPRYVELLVNVADESVMKFGADLEHYLLTLATARLYRHSILN 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 PPPEGSKTRSKRFYSEAFVETLLVADASMAAFYGTDLQNHILTVMSMAIRYKHPISRN 276
QY 261 PINIVYVAVLLLRDSDGPKTYGNALTLRNCAMOKKLNKYSKDKHPEYDIALTLFTROD 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 SVNLVYVAVLLIVERKMEPEVSDNGGLTLRNFCSMOKHNSPSDRPEYDIALTLFTROD 336
QY 321 LCG-ATTCDDTLGMADVCTMCDPKRSCSVIEDDGLPSAFTHAHELGHVFNPHDVKACEE 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 337 FCNGGEQCDTGMADVCTIOPDKSCSVIRKDEGLQAAVTLAHELGHVLSMHDQSKCYR 396
QY 380 VFGKLRANHMSPTLIQIDRANPWSACSAIITDFLDGHDCLLDPSKPSISPELDPG 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 LFGPMGXKHNMAPEFIHVNKTLPMSPCSAVYLTLLDGDHGDCLLDAPTSVLPPLTGPG 456
QY 440 AS--YTLSSQCELAFAVGSKPCP---YNQYCTKLMCTGKAKGQWVCOYTHF--PMDGTS 492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 HSTLYELDQOQKQTFGDPFRHCPTSVEDICVQLCARRDSDEYCTTKNSLMAAGTP 516
QY 493 CGEGKLCIKGACVDRHNLN--KHRDGSWAKMDPYGCSRTGCGGVOLARQCTNPTPAN 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 517 CGPHILCLDSCVLAKEDEVENKAVVDGDMGPMRWGQCSRTGCGGIQFNSNECDNPPRON 576
QY 551 GKATCEGVRAVYKSCNLEPCSSASGKSFREOCEAFNGYNHSTNRLTLAVAMVYKTSY 610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 577 GGRFCLEGRVYKQSCNTEECF--PNGKSFREOCEKYNAYNH--TDLGNFLOMWPKYSGV 633
QY 611 SPROCKLICRANGTYFYVLAAPKVVYDGLCPDSTSVYCGKCIKAGCDGMLSKKRPD 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 634-SPRDCRCLPCARGRSEKFAEAVVDGTLGCPDLSICVAGQCVKAGCDHVAVSPKLD 693
QY 671 KCGVCGDNKSCSKRVYTGFTKPMHGYNFVVALPAGASSIDIRORGYKGLIGDNTYALKN 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 694 KCGVCGGKGTACRKISSFPFSGYNDIYVTPAGATINIDVKQSHHPGVRNDGTYLAKT 753
QY 731 SQGKYLINGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILPEPLVEVLSV-GKM 789
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 754 ANGOYLLNGNLAIASIEDIIVKCTIILKYSGMATLERLSFQALPPLVYOLTLVSGEV 813
QY 790 TPRVRYSFVLPKPRRDSKSHRDPDGPVSLHNSVLSNOVEOPDPRPARVAGSWG 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 FPPKRYTFEVPND--MPSYONSKERATY--NIIOSL-----PSAEVNLQDMS 858
QY 850 PCSASGSGLOKRAYDRCGSAQRTVPACDAHRRPVTOAG-EPKP 895
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 859 ECPSTCGSMQRRTVECDRPSGQAS-DTCDEALKPEAKKCGSGPCP 904

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RESULT 13  
 ; Sequence 2, Application US/09972467  
 ; Patent No. US20020090373A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEIER INC.  
 ; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; FILE REFERENCE: PCI0850A  
 ; CURRENT APPLICATION NUMBER: US/09/972.467  
 ; CURRENT FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 1629  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-972-467-2

Query Match 38.1%; Score 1965; DB 10; Length 1629;  
 Best Local Similarity 39.9%; Pred. No. 7.7e-132;  
 Matches 411; Conservative 145; Mismatches 351; Indels 122; Gaps 21;

QY 22 EREVVPRLDP-----DINGRRYV-----RGPEDSGQGLIFQITAFQ 61  
 DB 47 EYEIPIRVNVLGEPEPTNVHFKTRRSINATDPMFAFASSSSSTSOAHYRLSAG 106  
 QY 62 EDVYHLTPDAQFLAPAESTEHLGVP---LQGLTGSSDLRCFCYSGDVNAEPDSFAV 117  
 DB 107 QOFLFLTNAGFIAPLFTVTLGTPGVNQTKFYSEEAELKHCFKGYGVNTNSEHTAVI 166  
 QY 118 SLGGLRGAFGRGAIEYISPLPNASAPAAQNSOGAHLQORGVGSGSOPTSQCYA 177  
 DB 167 SLCSGMLGFRSHDGYFTFPLQSMDEQDEEQNKPHILYRSAPQRPSTGRACOTS 226  
 QY 178 SGMNPAILLALDPYKPRAGFGE-----SRSHRSG 208  
 DB 227 EHKN---RHSKKKKTRAKMGERINLADVALNSGLATEAFSAVGNKTDTRREKTRH 283  
 QY 209 RAKREYSIRYVELTVADENSVKREHGADELHLLTLTAARLYNHSILNPINIVYK 268  
 DB 284 RKRRELSYRFEVLLVADNRVSYGEMLOHYITLMSIVASYDPSIGNLINIVYV 343  
 QY 269 VLLLRDSDPKYVTGNAALTLNFCAMOKKLNKVSDBHEYMDTALFTRODLGCA-TTC 327  
 DB 344 LIVIHNEODGPSISFMAOTTLKFCOMQHSKNSPGSIH---HDTAVLLTRDODICRAHDKC 400  
 QY 328 DTLGMAVGTMCDPKRSCEVEDDGLPSAFTTAHELGHVFNMPHDNVKCEEVFGKLRAN 387  
 DB 401 DTLGLAELGTICDPYKSCISEDSGLSTAFTIAHELGHVFNMPHDNNCKKEE-GVKSPO 459  
 QY 388 HMASPLIIDIRANPWASACSAIITDFLDSHGDCLLDP-SKPISLPREDPAGASTLSQ 446  
 DB 460 HMAPLPLNLYTPNMMWSKSRKYTEFTLDTYGECLLNBPESRPYLPOLPGLILNVNK 519  
 QY 447 OCELAFGVSKPCPYQYCTKLWC---TGKAGOMVCOYTRHPMADTSCGSEKCLKA 503  
 DB 520 OCELITGPPSOYCYMOCRLMKNVNVHKG---CRQHPMAAGTCEPEKHKHXYG 576  
 QY 504 CVERHNLNKHRYDGSWAKWDPYGPCSRITCGGGVOLAAROCNTPTPANGSKYCEGVVYK 563  
 DB 577 CVPK -EMDVPVTDGWSGSSPFGTCSRTCGGGIKTAIRCNRPKPKNGKCYGVGRMKK 635  
 QY 564 SCNLEPCPSASGKSFREOQCEAFNXYNSTNRLTLAVMVPKYSVSRBDKCKLGRAN 623  
 DB 636 SCNTEPCCLKOK--RDFRDOCAHFDEKHNINGLLRNVMPVPSGLIMDKRCLFCRYA 693  
 QY 624 GGYVFLAPKYVDTGLCPDSTSVYCGKCIKAGCDGNLGSKRRDKCGVCGGDKKSC 683  
 DB 694 GNTAYQLADRDYIDGTTPCCODTNDICVGLCKRAGCDHNLNSARDKCGCYCGGDNSSCK 753  
 QY 684 KYTGLFTKPMHGYNFVAIPAGASSIDIRORGYKGLIGDNTYLALKNSOQKYLNGHFVY 743

DB 754 TVAGTFNTVHYGYNVRLPRAGATNIDVRQHSFSETDDNDLALSSSGEFLNGNFV 813  
 QY 744 SAVERDLVYKGLLRYSGTGAVESLQASRPILPELVYVLSVGMTPRVRYSFLPKE 803  
 DB 814 TMAKREIRIGNAVYSESGEYVERLNSDRIEQLLQVLSVYKLYNPDVRYSPNIPLE 873  
 QY 804 PREDK--SSHPKDRGP-----SVLHNSVLSLNOVEQDDPP-- 840  
 DB 874 DKPQGFYWNHSH-----GPMQACSKPCQGERKKRLVCTRESQDLPVS---DQRCDRLPQ 925  
 QY 841 -----ARWVAGSWGPCSASCAGSGLQKRAVDCR-----GSAGRTVPACDAHR 883  
 DB 926 HTEPCGTDCLDRMNVASSECSAOCGLYRLDLYCAKYSRLDKTEKVDGFCSSHPK 985  
 QY 884 PVETQACGEPCPT--WEISAMSPCSKSGCGFORSLKCVGHGRLARDQCNLHRKPOE 941  
 DB 986 PSNREKSGECNTGWMRYSAMTECSKSCDGTQRRALCVNTRNDVLDOSKCT-HQEKVT 1044  
 QY 942 LDPCYLAPC 950  
 DB 1045 IORCSEFPC 1053

RESULT 14  
 ; US-10-174-590-352  
 ; Sequence 352, Application US/10174590  
 ; Publication No. US20030008352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430RCA42  
 ; CURRENT APPLICATION NUMBER: US/10/174,590  
 ; CURRENT FILING DATE: 2002-06-18  
 ; Prior application removed - See file wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 352  
 ; LENGTH: 837  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-174-590-352

Query Match 37.1%; Score 1916; DB 9; Length 837;  
 Best Local Similarity 46.3%; Pred. No. 1e-128;  
 Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

QY 1 MLILGLTLAPAGRTAGPEPEPEVVPYRLDPDINGRRYVWMPEDSGQGLIFQITAF 60  
 DB 37 LILLILASLPLPSARLASPLPREELVFPKLSVY-----PSGAPARLLCRLQAF 88  
 QY 61 OEDFVYHLTPDAQFLAPAESTEHLGVPLOGLTGSSDLRCFCYSGDVNAEPDSFAVSLC 120  
 DB 89 GETLLLELDSDSGVEGYEGLVYGLQGAPE-LLGGAEP--GYTLTGITINGDPESVASLHMD 145  
 QY 121 GG-LRGAFTGRGAIEYISPLPNASAPAAQNSOGAHLQORGVGSGSOPTSQCYA 179  
 DB 146 GGALLGVLQYRGAEHLQPLEGGTPNSA--GGPGAHILRRK---SPASQGFMCNV--- 196  
 QY 180 MNPAILLALDPYKPRAGGSESRRSRGRARKEVSIIPRYETLVYVADENSVKREHGADEL 239  
 DB 197 -----KAPLGSFSPRPR--RAKRFASLSFVETLVVADDMAAFHAGGLK 239

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QY 240 HYLLTLTAARLRHPSILNPINIVVYKLLLRDSDGPKVYTGNAALTLRNFCAWOKKL 299
DB 240 RYLLTVMAAAKAFKHSIRNPVSLVYRLVILSGSEGGPOVGPSPAQTLRSFCAMQKGL 299
QY 300 NKVSDKHPEYMDTALFLTRDLCGATTCDTLGMADVGMCPKRSQSVIEDGLPSAFTT 359
DB 300 NTPEDSGPDHEDTALFLTRDLCGATTCDTLGMADVGMCPKRSQSVIEDGLPSAFTT 359
QY 360 AHELGHEVNMHNDVYKCEEVFGKL-RANHMSPITLQIDRANPMSACSAIITDFLDSG 418
DB 360 AHELGHEVNMHNDVYKCEEVFGKL-RANHMSPITLQIDRANPMSACSAIITDFLDSG 418
QY 419 HGCDLLDPSKPISLPEDLPGASTLTSQCELAGVSGKPCPYM-QYCTKIMCTGKAKQ 477
DB 419 HGCDLLDPSKPISLPEDLPGASTLTSQCELAGVSGKPCPYM-QYCTKIMCTGKAKQ 477
QY 478 MWCOTRHPMADGTSCGSGKCLCKACVYERHNLKHNVD--GSAKKMPDPCSRCTGCGG 535
DB 478 MWCOTRHPMADGTSCGSGKCLCKACVYERHNLKHNVD--GSAKKMPDPCSRCTGCGG 535
QY 536 VOLARROCTNPTPANGKYGKCEGVYKYSNLEPCSSASGKSFREOCFAFNQYNHSTN 595
DB 536 VOLARROCTNPTPANGKYGKCEGVYKYSNLEPCSSASGKSFREOCFAFNQYNHSTN 595
QY 540 VQSSRDCTRPVNRNGKYGKCEGRTRFRSCNTEDCP-TGSALTFRRECCAA--YNHRTD 595
DB 540 VQSSRDCTRPVNRNGKYGKCEGRTRFRSCNTEDCP-TGSALTFRRECCAA--YNHRTD 595
QY 596 RLTL---AVANVPKYSVSPDKCKLICRANGTGYFYVLAIRVYDGLTSPDSTISCVQ 652
DB 596 RLTL---AVANVPKYSVSPDKCKLICRANGTGYFYVLAIRVYDGLTSPDSTISCVQ 652
QY 596 LKSPFGPMDVPRYTGVAPODCKLTCQARALGYVYVLEPRVYDGTFCPSDSSVCVOG 655
DB 596 LKSPFGPMDVPRYTGVAPODCKLTCQARALGYVYVLEPRVYDGTFCPSDSSVCVOG 655
QY 653 KCIRAGCDGNLGSKKRPKCGVCGDNKSCKVTGLFTKPMHGYNFVAIPAGASSIDIR 712
DB 653 KCIRAGCDGNLGSKKRPKCGVCGDNKSCKVTGLFTKPMHGYNFVAIPAGASSIDIR 712
QY 713 QRGYKGLIGDNYLALKNQSKYLLNGHFVYSAVERDLVYKGL-LRYSGTGAVESLQA 771
DB 713 QRGYKGLIGDNYLALKNQSKYLLNGHFVYSAVERDLVYKGL-LRYSGTGAVESLQA 771
QY 716 QQGNPG--HRSIYALALKLPDGSYALNGEYTLMPSTDVVLEGAVALRSATASETLISG 773
DB 716 QQGNPG--HRSIYALALKLPDGSYALNGEYTLMPSTDVVLEGAVALRSATASETLISG 773
QY 772 SRPLLEPLTVYVLSGKMTPRVRYVSFLPEKEPEDKSSHPKD 814
DB 772 SRPLLEPLTVYVLSGKMTPRVRYVSFLPEKEPEDKSSHPKD 814
QY 774 HGPLAQPLTLQVLAAGNPQDTRLRYSFVPRPTSTPRPTPD 816
DB 774 HGPLAQPLTLQVLAAGNPQDTRLRYSFVPRPTSTPRPTPD 816

RESULT 15
US-10-176-758-352
; Sequence 352, Application US/10176758
; Publication No. US2003008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-352

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Query Match 37.1%; Score 1916; DB 9; Length 837;  
 Best Local Similarity 46.3%; Pred. No. 1e-128;  
 Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

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QY 1 MLLGILTLAAGTAGGFEEREYVYPIRLDPDINGRRYRMRGPEDSGDLJFOITAF 60
DB 37 LLLLLIALLSARLASLPREEEIVPEKINGSVL-----PGSAPARLLCRLQAF 88
QY 61 QEDRIHLTPDAQTLAPFSTHEHGLVPLQGLTGSSDLRCFYGVDVAEDSAANSLC 120
DB 89 GETLLELEODSGVQVEGLIYVYLGQAE-LLGAEP--GTYLGTINGDESVASHMD 145
QY 121 GG-LRGAGYGAEEVISPLPNASAPAAQRNSOGAHLIQRGVGSGDPTSCGVAAS 179
DB 146 GGALLGVLYQYGAELHLIQLLEGTPNSA--GGPAHLIRK-----SPASGGPMCAV--- 196
QY 180 WNPALRALDPEYKRRAGFESRSRRSGRAKRPVSIPIRYETLVVADESNVKEHADLE 239
DB 197 -----KALGSPSPRR--RAKRRASLSRFETLVVADDDKMAAHGAGLK 239
QY 240 HYLLTLTAARLRHPSILNPINIVVYKLLLRDSDGPKVYTGNAALTLRNFCAWOKKL 299
DB 240 RYLLTVMAAAKAFKHSIRNPVSLVYRLVILSGSEGGPOVGPSPAQTLRSFCAMQKGL 299
QY 300 NKVSDKHPEYMDTALFLTRDLCGATTCDTLGMADVGMCPKRSQSVIEDGLPSAFTT 359
DB 300 NTPEDSGPDHEDTALFLTRDLCGATTCDTLGMADVGMCPKRSQSVIEDGLPSAFTT 359
QY 360 AHELGHEVNMHNDVYKCEEVFGKL-RANHMSPITLQIDRANPMSACSAIITDFLDSG 418
DB 360 AHELGHEVNMHNDVYKCEEVFGKL-RANHMSPITLQIDRANPMSACSAIITDFLDSG 418
QY 419 HGCDLLDPSKPISLPEDLPGASTLTSQCELAGVSGKPCPYM-QYCTKIMCTGKAKQ 477
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QY 478 MWCOTRHPMADGTSCGSGKCLCKACVYERHNLKHNVD--GSAKKMPDPCSRCTGCGG 535
DB 478 MWCOTRHPMADGTSCGSGKCLCKACVYERHNLKHNVD--GSAKKMPDPCSRCTGCGG 535
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DB 536 VOLARROCTNPTPANGKYGKCEGVYKYSNLEPCSSASGKSFREOCFAFNQYNHSTN 595
QY 540 VQSSRDCTRPVNRNGKYGKCEGRTRFRSCNTEDCP-TGSALTFRRECCAA--YNHRTD 595
DB 540 VQSSRDCTRPVNRNGKYGKCEGRTRFRSCNTEDCP-TGSALTFRRECCAA--YNHRTD 595
QY 596 RLTL---AVANVPKYSVSPDKCKLICRANGTGYFYVLAIRVYDGLTSPDSTISCVQ 652
DB 596 RLTL---AVANVPKYSVSPDKCKLICRANGTGYFYVLAIRVYDGLTSPDSTISCVQ 652
QY 596 LKSPFGPMDVPRYTGVAPODCKLTCQARALGYVYVLEPRVYDGTFCPSDSSVCVOG 655
DB 596 LKSPFGPMDVPRYTGVAPODCKLTCQARALGYVYVLEPRVYDGTFCPSDSSVCVOG 655
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DB 653 KCIRAGCDGNLGSKKRPKCGVCGDNKSCKVTGLFTKPMHGYNFVAIPAGASSIDIR 712
QY 713 QRGYKGLIGDNYLALKNQSKYLLNGHFVYSAVERDLVYKGL-LRYSGTGAVESLQA 771
DB 713 QRGYKGLIGDNYLALKNQSKYLLNGHFVYSAVERDLVYKGL-LRYSGTGAVESLQA 771
QY 716 QQGNPG--HRSIYALALKLPDGSYALNGEYTLMPSTDVVLEGAVALRSATASETLISG 773
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Search completed: April 29, 2003, 17:21:45  
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